

FT	Protein	29.	.666	PP	22-DEC-1997; AU0874.
PN	WO9827805-A1.			PR	"note= "mature protein"
PD	02-JUL-1998.			PA	
PF	22-DEC-1997; AU0874.			(RETR)	COOP RES CENT TROPICAL PLANT PATHOLOGY.
DE	20-DEC-1996; AU-004275.			PI	Bower NI, Goulier KC, Green JL, Manners JM, Marcus JP;
OS	(RETR) COOP RES CENT TROPICAL PLANT PATHOLOGY.			DR	WPI: 98-37279/32.
PS	Bower NI, Goulier KC, Green JL, Manners JM, Marcus JP;			PT	Novel anti-microbial protein from e.g. Macadamia integrifolia - useful for controlling microbial infestations of plants or mammals
CC	N-PADB: V42310.			PS	WPI: 98-37279/32.
CC	Novel anti-microbial protein from e.g. Macadamia integrifolia - useful for controlling microbial infestations of plants or mammals			CC	Claim 1; Page 49-51; 96pp; English.
CC	Claim 1; Page 34-36; 96pp; English.			CC	The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and mammalian animals.
SQ	Sequence 666 AA;			SQ	Sequence 590 AA;
RESULT	3	100.0%	Score 361; DB 1; Length 666;	Query Match	30.2%; Score 109; DB 1; Length 590;
ID	W62830 standard; Protein; 625 AA.			Best Local Similarity 45.2%; Pred. No. 1 26e-02;	
AC	W62830;			Mismatches 6; Indels 1; Gaps 1;	
DT	27-OCT-1998 (first entry)			Matches 14; Conservative 14;	
DE	Macadamia integrifolia antimicrobial protein.			Indels 1; Gaps 1;	
OS	antimicrobial protein; infestation; control.			Mismatches 10; Sequence 590 AA;	
FH	Macadamia integrifolia.			Indels 1; Gaps 1;	
Key	Location/Qualifiers			Mismatches 6; Sequence 590 AA;	
FT	Peptide 1..28			Indels 1; Gaps 1;	
FT	/note= "signal peptide"			Mismatches 10; Sequence 590 AA;	
FT	protein 29..666			Indels 1; Gaps 1;	
FT	/note= "mature protein"			Mismatches 6; Sequence 590 AA;	
PN	WO9827805-A1.			Indels 1; Gaps 1;	
PD	02-JUL-1998.			Mismatches 10; Sequence 590 AA;	
PR	22-DEC-1997; AU0874.			Indels 1; Gaps 1;	
PP	20-DEC-1996; AU-004275.			Mismatches 6; Sequence 590 AA;	
PA	(RETR) COOP RES CENT TROPICAL PLANT PATHOLOGY.			Indels 1; Gaps 1;	
PI	Bower NI, Goulier KC, Green JL, Manners JM, Marcus JP;			Mismatches 6; Sequence 590 AA;	
DR	WPI: 98-37279/32.			Indels 1; Gaps 1;	
PT	Novel anti-microbial protein from e.g. Macadamia integrifolia - useful for controlling microbial infestations of plants or mammals			Mismatches 6; Sequence 590 AA;	
PS	Claim 1; Page 47-49; 96pp; English.			Indels 1; Gaps 1;	
CC	The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and mammalian animals.			Mismatches 6; Sequence 590 AA;	
CC	Sequence 525 AA;			Indels 1; Gaps 1;	
SQ	Sequence 625 AA;			Mismatches 6; Sequence 590 AA;	
RESULT	4	71.7%	Score 259; DB 1; Length 625;	Query Match	26.9%; Score 97; DB 1; Length 525;
ID	W62832 standard; Protein; 590 AA.			Best Local Similarity 31.4%; Pred. No. 1 88e-01;	
AC	W62832;			Mismatches 11; Indels 1; Gaps 1;	
DT	27-OCT-1998 (first entry)			Matches 11; Conservative 11; Indels 1; Gaps 1;	
DE	Gossypium hirsutum antimicrobial protein.			Mismatches 12; Indels 1; Gaps 1;	
OS	antimicrobial protein; infestation; control.			Sequence 525 AA;	
PS	Gossypium hirsutum.			Sequence 590 AA;	
PN	WO9827805-A1.			Sequence 590 AA;	
PD	02-JUL-1998.			Sequence 590 AA;	
PR	22-DEC-1997; AU0874.			Sequence 590 AA;	
PA	"note= "mature protein"			Sequence 590 AA;	
PI				Sequence 590 AA;	
DR				Sequence 590 AA;	
PT				Sequence 590 AA;	
PS				Sequence 590 AA;	
CC				Sequence 590 AA;	
RESULT	5	100.0%	Score 361; DB 1; Length 525;	Query Match	30.2%; Score 109; DB 1; Length 590;
ID	W62831 standard; Protein; 525 AA.			Best Local Similarity 45.2%; Pred. No. 1 26e-02;	
AC	W62831;			Mismatches 6; Indels 1; Gaps 1;	
DT	27-OCT-1998 (first entry)			Matches 14; Conservative 14;	
DE	Theobroma cacao antimicrobial protein.			Indels 1; Gaps 1;	
KW	Theobroma cacao.			Mismatches 10; Sequence 590 AA;	
OS	Theobroma cacao.			Indels 1; Gaps 1;	
PS	W09827805-A1.			Mismatches 6; Sequence 590 AA;	
CC	22-DEC-1997; AU0874.			Indels 1; Gaps 1;	
CC	20-DEC-1996; AU-004275.			Mismatches 6; Sequence 590 AA;	
SQ	Sequence 590 AA;			Indels 1; Gaps 1;	
RESULT	6	100.0%	Score 361; DB 1; Length 525;	Query Match	26.9%; Score 97; DB 1; Length 525;
ID	R20181 standard; Protein; 566 AA.			Best Local Similarity 31.4%; Pred. No. 1 88e-01;	
AC	R20181;			Mismatches 11; Indels 1; Gaps 1;	
DT	16-APR-1992 (first entry)			Matches 11; Conservative 11; Indels 1; Gaps 1;	
DE	Sequence encoded by 67 kD T. cacao protein cDNA.			Mismatches 12; Indels 1; Gaps 1;	
KW	Cocoa; flavour; vicilin; seed storage protein.			Sequence 525 AA;	
OS	Theobroma cacao.			Sequence 590 AA;	
PS	W0919801-A.			Sequence 590 AA;	
CC	26-DEC-1991.			Sequence 590 AA;	
CC	07-JUN-1991; GB00914			Sequence 590 AA;	
CC	11-JUN-1990; GB-013316.			Sequence 590 AA;	
PT	(MRSC) MARS UK LTD.			Sequence 590 AA;	
PI	Spencer ME, Hodge R, Deakin EA, Ashton S;			Sequence 590 AA;	
DR	WPI: 92-034418/03.			Sequence 590 AA;	
PT	Recombinant cocoa proteins - are responsible for flavour in cocoa beans and produced in large quantities using yeast and bacterial expression vectors.			Sequence 590 AA;	
OS	Claim 4; Fig 2; 59pp; English.			Sequence 590 AA;	
PS	The inventors claim a 67 kD and 31 kD T. cacao protein, and			Sequence 590 AA;	
CC	WO9827805-A1.			Sequence 590 AA;	
CC	02-JUL-1998.			Sequence 590 AA;	

CC fragments, and encoding DNAs. The 47 kD and 31 kD proteins are derived from the 67 kD precursor. *T. cacao* protein cDNA was detected in a cDNA library prepared from immature cocoa beans RNA using a probe based on the AA sequence of a Cmbr peptide common to the 47 kD and 31 kD polypeptides. Homology searches revealed close homologues between the 67 kD polypeptide and the vicilins, which are seed storage proteins.

Sequence 366 AA;

Query Match 26.9%; Score 97; DB 1; Length 565;
Best Local Similarity 31.4%; Pred. No. 1.88e-01;
Matches 11; Conservative 11; Mismatches 12; Indels 1; Gaps 1;

Db 39 ROQEQQCORCSEATEEREQFOEQRCEREREKQ 73
Qy 33 ROEYEECKRQCMOLEMSGQMR-RCVSQCDKFEED 66

RESULT 7

ID W40287 standard; Protein; 218 AA.

AC W40287;

DT 18-AUG-1998 (first entry)

DE Human TSPL protein.

KW TSPL; thrombospondin; anti-angiogenic; cationic vehicle; gene therapy;

metabolic disease; tumour.

OS Homo sapiens.

FH Misc_difference 160

FT Misc_difference 217

FT peptide 12.27

FT /label= anti-angiogenic peptide 142.-159

FT Peptide 199

FT /label= anti-angiogenic peptide 217

FT EP-819758-A2.

FT PD 21-JAN-1998

FT PF 16-JUL-1997; 112154-

FT PR 16-JUL-1996; US 680845.

FT PA (MIXS/.) MIXSON A J.

FT PI

FT DR WPI; 98-078839/08.

FT PT Mixson AJ;

FT PS DR-PSDB; V10493.

PT Complexes of DNA encoding anti-angiogenic peptide - with cationic liposome(s) or cationic polymer, useful for, e.g. gene therapy of tumours

PT Claim 9: Page 6; 47pp; English.

CC This sequence represents the thrombospondin gene TSPL which is used in a method to produce a cationic vehicle consisting of a cationic liposome:DNA complex where the DNA encodes an anti-angiogenic peptide or tumour suppressor protein. Such complexes are used for treatment of neoplastic and metabolic diseases especially for gene therapy of tumours.

SO Sequence 218 AA;

Query Match 26.3%; Score 95; DB 1; Length 218;

Best Local Similarity 50.0%; Pred. No. 2.93e-01;

Matches 12; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

RESULT 8

ID R40823 standard; protein; 239 AA.

AC R40823;

DT 03-MAR-1994 (first entry)

DE Human thrombospondin 1.

KW hTSP-1; platelet glycoprotein; angiogenesis; neovascularisation; inhibitor; solid tumour; skin cancer; angiogenic dysfunction;

KW melanoma; diabetic retinopathy; psoriasis; neovascular glaucoma; Kaposi's sarcoma; inflammation; retrosternal fibroplasia.
KW Homo sapiens.
OS Homo sapiens.
PN WO9316716-A.
PD 02-SEP-1993.
PF 22-FEB-1993; US01652.
PR (NOUN) UNIV NORTHWESTERN.
PI BOUCK NP, Frazer WA, Good DJ, Polverini PJ;
DR WPI; 93-28818/56.
PT Compn. for inhibiting angiogenesis - contg. a vascularisation inhibitor comprising a peptide capable of inhibiting
PT vascularisation
PS Claim 10; Page 41-42; 51pp; English.
CC Certain fragments of thrombospondin, a glycoprotein found in the
alpha granules of platelets, can inhibit vascularisation. Peptides
derived from the hTSP sequence are useful for inhibiting
neovascularisation, esp. in solid tumours such as melanomas. The
inhibitory peptides can also be used in other diseases involving
CC angiogenic dysfunction. See R40824-R40830.

Query Match 26.3%; Score 95; DB 1; Length 239;
Best Local Similarity 50.0%; Pred. No. 2.93e-01;
Matches 12; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

Db 105 SSVQTTRCHIGBCDKPKQDGWS 128
Qy 48 TSGQMRC-VSQCDKFEEDDW 70

Query Match 9

Best Local Similarity 50.0%; Pred. No. 2.93e-01;

Matches 12; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

RESULT 9

ID W40288 standard; Protein; 441 AA.

AC W40288;

DT 18-AUG-1998 (first entry)

DE Human concatameric TSPL protein.

KW TSPL; thrombospondin; anti-angiogenic; cationic vehicle; gene therapy;

KW liposome; DNA complex; tumour suppressor protein; treatment; neoplastic;

KW metabolic disease; concatamer; tumour.

OS Homo sapiens.

FH Synthetic.

FH Key Difference 160

FT Misc_difference /note= "encoded by CGG" 221

FT FT Misc_difference /note= "encoded by GAC" 383

FT FT Misc_difference 383

FT /note= "encoded by CGG"

FT Region 223.-227 intervening sequence

FT PN EP-819758-A2.

FT PD 21-JAN-1998

FT PF 16-JUL-1997; 112154-

FT PR 16-JUL-1996; US 680845.

FT PA (MIXS/.) MIXSON A J.

FT PI Mixson AJ;

FT DR WPI; 98-078839/08.

FT PT Complexes of DNA encoding anti-angiogenic peptide - with cationic liposome(s) or cationic polymer, useful for, e.g. gene therapy of tumours

FT Claim 9; Page 6-7; 47pp; English.

CC This protein sequence represents a concatamer of thrombospondin TSPL which is used in a method to produce a cationic vehicle consisting of a cationic liposome:DNA complex where the DNA encodes an anti-angiogenic peptide or tumour suppressor protein. Such complexes are used for treatment of neoplastic and metabolic diseases especially for gene therapy of tumours.

SO Sequence 441 AA;

Query Match 26.3%; Score 95; DB 1; Length 441;

Best Local Similarity 50.0%; Pred. No. 2.93e-01;

Matches 12; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

Db 116 SSVORTCHIQEQCDKRFKODGGS 139
 ID W03698; standard; Protein: 62 AA.
 AC W03698;
 DT 06-MAR-1997 (first entry)
 DE Maize Id gene product.
 KW Maize; Zea mays; Id; id*; transposon; transposable element;
 OS Zea mays.
 PN W0933408A2.

PD 31-OCT-1996.

PF 15-MAR-1996; U03466
 PR 15-MAR-1995; US-400186.
 PA (COLD-) COLD SPRING HARBOR LAB.
 PI Colasanti, JJ; Sundaresan V;
 DR WPI; 96-497621/49.

DRPDB; T412174; T41175.

New isolated plant Id gene - used to develop prods. for use in altering the induction of flowering in Plants
 PT Claim 7; Fig 3 and Fig 5; 58pp; English.
 CC The Id gene controls flower evocation in maize plants. The maize nucleic acid is similar to that of genes encoding zinc-finger regulatory proteins in animals.

CC Transposons Ac and Ds constitute a family of related transposable elements present in maize. A derivative of Ds, Ds2, can be used to produce a new mutant of the Id gene. The Ds2 (in the presence of active Ac) is excised from a nearby gene on chromosome 1 and inserted into the Id gene to produce id*.

Sequence 62 AA;

Query Match 21.3%; Score 77; DB 1; Length 62;
 Best Local Similarity 35.0%; Pred. No. 1.39e+01;
 Matches 7; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Db 17 GEKRWCCERCGKPYAVQSDW 36
 ID :::::|:|:|:||:||:
 Oy 50 GQMRCVSCQCDKRFEDIDW 69

PT Result 10
 ID W03698 standard; Protein: 62 AA.
 AC W03698;
 DT 06-MAR-1997 (first entry)
 DE Maize Id gene product.
 KW Maize; Zea mays.

OS Zea mays.
 PN W0933408A2.

PR 15-MAR-1996; U03466
 PA (COLD-) COLD SPRING HARBOR LAB.

PI Colasanti, JJ; Sundaresan V;
 DR WPI; 96-497621/49.

DRPDB; T412174; T41175.

New isolated plant Id gene - used to develop prods. for use in altering the induction of flowering in Plants
 PT Claim 7; Fig 3 and Fig 5; 58pp; English.

CC The Id gene controls flower evocation in maize plants. The maize nucleic acid is similar to that of genes encoding zinc-finger regulatory proteins in animals.

CC Transposons Ac and Ds constitute a family of related transposable elements present in maize. A derivative of Ds, Ds2, can be used to produce a new mutant of the Id gene. The Ds2 (in the presence of active Ac) is excised from a nearby gene on chromosome 1 and inserted into the Id gene to produce id*.

Sequence 62 AA;

Query Match 21.3%; Score 77; DB 1; Length 62;
 Best Local Similarity 35.0%; Pred. No. 1.39e+01;
 Matches 7; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Db 17 GEKRWCCERCGKPYAVQSDW 36
 ID :::::|:|:|:||:||:
 Oy 50 GQMRCVSCQCDKRFEDIDW 69

PT Result 11
 ID W90342 standard; protein: 409 AA.
 AC W90342;
 DT 24-MAY-1999 (first entry)

DE G. max truncated SBP2 protein.
 KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant; seed; carbohydrate content; soybean.

OS Glycine max.
 PN W0935308A1.

PD 25-NOV-1998.
 PF 21-MAY-1998; U10465.
 PR 22-MAY-1997; US-047568.
 PA (UNIV) UNIV WASHINGTON STATE RES FOUND.
 PI Chao WS, Grimes HD;
 DR WPI; 99-070155/06.

PT New modified plant sucrose binding proteins - used to develop transgenic plants which can have enhanced or decreased sucrose uptake activity in developing seeds

PT This sequence represents a novel sucrose binding protein, SBP2 isolated from Glycine max. This protein is used in a method resulting in the production of a modified plant sucrose binding protein (SBP), which has a modified amino acid sequence compared to a corresponding wild-type SBP, and where expression of the modified SBP in a yeast assay system confers enhanced sucrose uptake compared to the corresponding wild-type SBP. The products of the invention can be used for producing transgenic plants which have modified sucrose uptake activity, particularly in developing seeds. Enhanced sucrose uptake activity in developing seeds may be desirable where it is an advantage to increase the carbohydrate content

CC of the seed (e.g. where the seed is the primary plant material harvested, such as soybean). In contrast, decreased sucrose uptake activity in seeds might be desirable where the vegetative material of the plant is harvested. The SBP regulatory regions confer specific or enhanced expression in developing seeds and so may be used to express any transgene in developing seeds.

Sequence 409 AA;

RESULT 12
 ID W59836 standard; Protein: 438 AA.
 AC W59836;
 DT 16-Nov-1998 (first entry)
 DE Maize Id protein.
 KW Maize; Id; floral induction; transgenic plant.
 OS Zea mays.
 PN W0937201-A1.
 PD 27-AUG-1998.
 PR 18-FEB-1998; U03161.
 DR 30-DEC-1997; US-000640.
 PT 20-FEB-1997; US-804104.
 PA (COLD-) COLD SPRING HARBOR LAB.
 PI Colasanti, JJ; Sundaresan V;
 DR WPI; 98-467564/40.
 N-FSDB; .V41721.

PT Id gene controlling floral induction in maize - useful to create transgenic plants with earlier, delayed or inhibited floral induction e.g. to extend geographical range of crops

PT Claim 5; Fig 3; 88pp; English.

The maize Id gene controls floral induction and is useful in the production of transgenic plants with altered floral induction times, i.e. earlier, delayed or inhibited floral induction. The Id gene and zinc-finger regulatory regions are useful to identify these genes in maize and isolate similar genes in other plants. The polypeptides and antibodies are also useful in Id detection e.g. to locate activity in CC plants.

Sequence 438 AA;

Query Match 21.3%; Score 77; DB 1; Length 438;
 Best Local Similarity 35.0%; Pred. No. 1.39e+01;
 Matches 7; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Db 187 GEKRWCCERCGKPYAVQSDW 206
 ID :::::|:|:|:||:||:
 Oy 50 GQMRCVSCQCDKRFEDIDW 69

PT Result 13
 ID W90340 standard; protein: 444 AA.
 AC W90340;
 DT 24-MAY-1999 (first entry)

DE G. max truncated SBP1 protein.
 KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant; seed; carbohydrate content; soybean.

OS Glycine max.
 PN W085308A1.

PD 26-NOV-1998.
 PF 21-MAY-1998; U10465.
 PR 22-MAY-1997; US-047568.
 PA (UNIV) UNIV WASHINGTON STATE RES FOUND.
 PI Chao WS, Grimes HD;
 DR WPI; 99-070155/06.

PT New modified plant sucrose binding proteins - used to develop transgenic plants which can have enhanced or decreased sucrose uptake activity in developing seeds

Page
5

PS
CC Claim 7; Page 36-37; 58pp; English.
CC This sequence represents a novel sucrose binding protein, SBP1 isolated
CC from Glycine max. This protein is used in a method resulting in the
CC production of a modified plant sucrose binding protein (SBP) which has a
CC modified amino acid sequence compared to a corresponding wild-type SBP,
CC and where expression of the modified SBP in a yeast assay system confers
CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
CC The products of the invention can be used for producing transgenic plants
CC which have modified sucrose uptake activity, particularly in developing
CC seeds. Enhanced sucrose uptake activity in developing seeds may be
CC desirable where it is an advantage to increase the carbohydrate content
CC of the seed (e.g. where the seed is the primary plant material harvested
CC such as soybean). In contrast, decreased sucrose uptake activity in
CC seeds might be desirable where the vegetative material of the plant is
CC harvested. The SBP regulatory regions confer specific or enhanced
CC expression in developing seeds and so may be used to express any
CC transgene in developing seeds.
Sequence 444 AA;
SQ

ULT. 15
W90339 standard; protein: 524 AA.
W90339;
24-MAY-1999 (first entry)
G max SBP1 protein.
SBP1: sucrose binding protein; SBP2: sucrose uptake: transgenic plant;
seed; carbohydrate content; soybean.
glycine max.
WO9851086-A1.
26-NOV-1998.
21-MAY-1998: U10465.
22-MAY-1997; US-047568.
(UNIW) UNIV WASHINGTON STATE RES FOUND.
Chao WS, Grimes HD;
WPI: 99-070155/06.
New modified plant sucrose binding proteins - used to develop
transgenic plants which can have enhanced or decreased sucrose

	Query Match	Best Local Similarity	Score	DB 1;	Length
Db	CKHQCQQQQYTEGDKRVCLOCD	44.4%	21.3%	77;	444;
Oy	: : : : :	44.4%	21.3%	Pred. No. 1.399+01;	
	CKRQCMQLE--TSGMRRCVSQLDRE	44.4%	21.3%	Mismatches 6;	
	39	63		Indels 3;	
				Gaps 2;	

RESULT 14
 ID W00341 standard; protein: 489 AA.
 AC W90341;
 DT 24-MAY-1999 (first entry)
 DE G- max SBP2 protein.
 KW SBM1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
 seed; carbohydrate content; soybean.
 OS Glycine max.
 PN WO883006-A1.
 DD-Nov-1998

Search completed: Sat May 13 09:29:23 2000
Job time : 8 secs.

	Query	Match	21.3%	Score	77	DB	1	Length	524
Best	Local	Similarity	44.4%	Pred.	No.	1.39×10^{-1}	Mismatches	6	Indels
Matches	12;	Conservative							Gaps
Db	43	CKHOCOOQDQTYEGKRVQIQCSD- : : :	RY	68					
Ov	39	CKRQCMOLE--TSGOMRCQSQCRF	63						

